LISTING OF CLAIMS

Amendment to the Claims

This listing of claims will replace all prior versions, and listing, of claims in the application.

Please amend the claims as follows:

Claim 1 (withdrawn – currently amended): An isolated, synthetic or recombinant nucleic acid comprising:

~~(a) a nucleic acid sequence having at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% or complete sequence identity to SEQ ID NO:1 over a region of at least about 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1100, 1200, 1300, 1400, 1500, 1600 or 1700 residues, or the full length of SEQ ID NO:1,~~

~~a nucleic acid sequence having at least 55%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% or complete sequence identity to SEQ ID NO:3 over a region of at least about 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1100, 1200 or 1250 residues, or the full length of SEQ ID NO:3,~~

~~a nucleic acid sequence having at least 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% or complete sequence identity to SEQ ID NO:5 over a region of at least about 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1100, 1200, 1300, 1400, 1500, 1600, 1700, 1800 residues, or the full length of SEQ ID NO:5,~~

~~a nucleic acid sequence having at least 95%, 96%, 97%, 98% or 99% or complete sequence identity to SEQ ID NO:7 over a region of at least about 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1100, 1200, 1300, 1400, 1500, 1600, 1700, 1800, 1900, 2000, 2100, 2200, 2300 residues, or the full length of SEQ ID NO:7,~~

a nucleic acid sequence having at least ~~60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%,~~ 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% or complete sequence identity to SEQ ID NO:9 over a region of at least about 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1100, 1200, 1300, 1400, 1500, 1600 residues, or the full length of SEQ ID NO:9,

~~a nucleic acid sequence having at least 50%, 55%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97% 98% or 99% or complete sequence identity to SEQ ID NO:11 over a region of at least about 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1100, 1200, 1300, 1400, 1500, 1600, 1700 residues, or the full length of SEQ ID NO:11,~~

~~a nucleic acid sequence having at least 50%, 55%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% or complete sequence identity to SEQ ID NO:13 over a region of at least about 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1100, 1200, 1300, 1350 residues, or the full length of SEQ ID NO:13,~~

~~a nucleic acid sequence having at least 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% or complete sequence identity to SEQ ID NO:15 over a region of at least about 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1100, 1200, 1300, 1400, 1500, 1600 residues, or the full length of SEQ ID NO:15,~~

~~a nucleic acid sequence having at least 50%, 55%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% or complete sequence identity to SEQ ID NO:17 over a region of at least about 100, 150, 200, 250,~~

~~300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1100, 1200, 1300, 1350 residues, or the full length of SEQ ID NO:17,~~

~~a nucleic acid sequence having at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% or complete sequence identity to SEQ ID NO:19 over a region of at least about 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1100, 1200, 1300, 1400, 1500, 1600, 1650 residues, or the full length of SEQ ID NO:19,~~

~~a nucleic acid sequence having at least 95%, 96%, 97%, 98% or 99% or complete sequence identity to SEQ ID NO:21 over a region of at least about 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1100, 1200, 1300, 1400 residues, or the full length of SEQ ID NO:21, or~~

~~a nucleic acid sequence having at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% or complete sequence identity to SEQ ID NO:23 over a region of at least about 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1100, 1200, 1300, 1400, 1500, 1600, 1650 residues, or the full length of SEQ ID NO:23,~~

wherein the nucleic acid encodes at least one polypeptide having a glucosidase activity, and optionally the sequence identities are determined by analysis with a sequence comparison algorithm or by a visual inspection,

wherein optionally the sequence comparison algorithm is a BLAST version 2.2.2 algorithm where a filtering setting is set to blastall -p blastp -d "nr pataa" -F F, and all other options are set to default;

(b) a nucleic acid sequence encodes a polypeptide comprising the sequence of ~~SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8,~~ SEQ ID NO:10~~, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22 or SEQ ID NO:24~~;

(c) a nucleic acid sequence that hybridizes under stringent conditions to a nucleic acid comprising the sequence of ~~SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7,~~ SEQ ID NO:9~~, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21 or SEQ ID NO:23~~ or subsequences thereof,

wherein the nucleic acid encodes a polypeptide having a glucosidase activity, wherein optionally the nucleic acid is at least about 50, 75, 100, 150, 200, 300, 400, 500, 600, 700, 800, 900, 1000 or more residues in length or the full length of the gene or transcript, or optionally the stringent conditions include a wash step comprising a wash in 0.2.times.SSC at a temperature of about 65.degree. C. for about 15 minutes;

(d) a nucleic acid sequence fully complementary to (a), (b) or (c),

wherein optionally the glucosidase activity comprises an .alpha.-glucosidase activity, or the glucosidase activity comprises catalyzing the hydrolysis of an alpha-(1,4) glucose linkage, an alpha-(1,6) glucose linkage, an alpha-(1,2) glucose linkage, an alpha-(1,3) glucose linkage or a combination thereof, or the glucosidase activity comprises catalyzing the hydrolysis of alpha-(1,4) glucose linkages and alpha-(1,6) glucose linkages, or the glucosidase activity comprises hydrolyzing glucosidic bonds in a starch to produce maltodextrins, or the glucosidase activity comprises catalyzing the hydrolysis of both malto-oligosaccharides and liquefied starch, or the .alpha.-glucosidase activity comprises a 1,4-α-D-glucan hydrolase activity or a 1,6-α-D-glucan hydrolase activity, or the glucosidase activity comprises an exoglucosidase activity, or the α-glucosidase activity comprises hydrolyzing glucosidic bonds in a starch, or the glucosidase activity comprises catalyzing the hydrolysis of starch to alpha-D-glucose residues, or the glucosidase activity comprises cleaving a glucose residue from a reducing or a non-reducing end of a starch,

wherein optionally the glucosidase activity is thermostable, or the polypeptide retains a glucosidase activity under conditions comprising a temperature range of between about 37° C. to about 95° C., or wherein the polypeptide retains a glucosidase activity under conditions comprising a temperature range of between about 55 ° C. to about 85 ° C., between about 70 ° C. to about 95 ° C. or between about 90 ° C. to about 95 ° C.,

wherein optionally the glucosidase activity is thermotolerant, or the polypeptide retains a glucosidase activity after exposure to a temperature in the range from between about 37 ° C. to about 95 ° C., or the polypeptide retains a glucosidase activity after exposure to a temperature in the range from between about 55 ° C. to about 85 ° C. or between about 90 ° C. to about 95 ° C.

Claims 2 to 24 (canceled)

Claim 25 (withdrawn – currently amended): A nucleic acid probe for identifying or isolating a nucleic acid encoding a polypeptide with a glucosidase activity, wherein the probe comprises at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, 110, 120, 130, 150 or more consecutive bases of a sequence comprising (a) ~~SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7,~~ SEQ ID NO:9~~, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21 or SEQ ID NO:23~~, or (b) the sequence of claim 1, wherein the probe identifies or isolates the nucleic acid by binding or hybridization,

wherein optionally the probe comprises an oligonucleotide comprising at least about 10 to 50, about 20 to 60, about 30 to 70, about 40 to 80, about 60 to 100, or about 50 to 150 consecutive bases,

wherein optionally the probe comprises a nucleic acid comprising at least about 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, 110, 120, 130, 150 or more consecutive residues of a sequence comprising ~~SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7,~~ SEQ ID NO:9~~, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21 or SEQ ID NO:23~~.

Claims 26 to 28 (canceled)

Claim 29 (withdrawn - previously presented): An amplification primer sequence pair for amplifying a nucleic acid encoding a polypeptide having a glucosidase activity, wherein the primer pair is capable of amplifying a nucleic acid comprising the sequence of claim 1, or a subsequence thereof,

wherein optionally each member of the amplification primer sequence pair comprises an oligonucleotide comprising at least about 10 to 50 consecutive bases of the sequence.

Claims 30 to 31 (canceled)

Claim 32 (withdrawn - previously presented): An expression cassette comprising a nucleic acid comprising the sequence of claim 1.

Claim 33 (withdrawn - previously presented): A vector comprising a nucleic acid comprising the sequence of claim 1.

Claim 34 (withdrawn - previously presented): A cloning vehicle comprising a nucleic acid comprising the sequence of claim 1, wherein the cloning vehicle comprises a viral vector, a plasmid, a phage, a phagemid, a cosmid, a fosmid, a bacteriophage or an artificial chromosome,

wherein optionally the viral vector comprises an adenovirus vector, a retroviral vector or an adeno-associated viral vector, or optionally the viral vector comprises a bacterial artificial chromosome (BAC), a plasmid, a bacteriophage P1-derived vector (PAC), a yeast artificial chromosome (YAC), or a mammalian artificial chromosome (MAC).

Claims 35 to 36 (canceled)

Claim 37 (withdrawn - previously presented): An isolated or cultured transformed cell comprising a nucleic acid comprising the sequence of claim 1, or the expression cassette of claim 32,

wherein optionally the cell is a bacterial cell, a mammalian cell, a fungal cell, a yeast cell, an insect cell or a plant cell.

Claim 38 to 39 (canceled)

Claim 40 (withdrawn - previously presented) : A transgenic non-human animal comprising the sequence of claim 1, wherein optionally the animal is a mouse, a goat, a rabbit, a sheep, a pig, a cow or a rat.

Claim 41 (canceled)

Claim 42 (withdrawn - previously presented): A transgenic plant comprising the sequence of claim 1,

wherein optionally the plant is a corn plant, a sorghum plant, a potato plant, a tomato plant, a wheat plant, an oilseed plant, a rapeseed plant, a soybean plant, a rice plant, a barley plant, a grass, or a tobacco plant.

Claim 43 (canceled)

Claim 44 (withdrawn - previously presented): A transgenic seed comprising the sequence of claim 1,

wherein optionally the seed is a corn seed, a wheat kernel, an oilseed, a rapeseed, a soybean seed, a palm kernel, a sunflower seed, a sesame seed, a rice, a barley, a peanut or a tobacco plant seed.

Claim 45 (canceled)

Claim 46 (withdrawn - previously presented): An antisense oligonucleotide comprising a nucleic acid sequence complementary to or capable of hybridizing under stringent conditions to the sequence of claim 1, or a subsequence thereof,

wherein optionally the antisense oligonucleotide is between about 10 to 50, about 20 to 60, about 30 to 70, about 40 to 80, or about 60 to 100 bases in length.

Claim 47 (canceled)

Claim 48 (withdrawn - previously presented): A method of inhibiting the translation of an glucosidase message in a cell comprising administering to the cell or expressing in the cell an antisense oligonucleotide comprising a nucleic acid sequence complementary to or capable of hybridizing under stringent conditions to the sequence of claim 1.

Claim 49 (withdrawn - previously presented): A double-stranded inhibitory RNA (RNAi) molecule comprising a subsequence of the sequence of claim 1,

wherein optionally RNAi is about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29 or 30 or more duplex nucleotides in length.

Claim 50 (canceled)

Claim 51 (withdrawn - previously presented): A method of inhibiting the expression of an glucosidase in a cell comprising administering to the cell or expressing in the cell a double-stranded inhibitory RNA (iRNA), wherein the RNA comprises a subsequence of the sequence of claim 1.

Claim 52 (currently amended): An isolated, synthetic or recombinant polypeptide having glucosidase activity comprising:

~~(a) an amino acid sequence having at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% or complete sequence identity to SEQ ID NO:2 over a region of at least about 100, 150, 200, 250, 300, 350, 400, 450, 500, 550 residues, or the full length of SEQ ID NO:2,~~

~~an amino acid sequence having at least 55%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% or complete sequence identity to SEQ ID NO:4 over a region of at least about 100, 150, 200, 250, 300, 350, 400 residues, or the full length of SEQ ID NO:4,~~

~~an amino acid sequence having at least 65% sequence identity to SEQ ID NO:6 over a region of at least about 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600 residues, or the full length of SEQ ID NO:6,~~

~~an amino acid sequence having at least 95% sequence identity to SEQ ID NO:8 over a region of at least about 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750 residues, or the full length of SEQ ID NO:8,~~

an amino acid sequence having at least [[60%]] 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% or complete sequence identity to SEQ ID NO:10 over a region of at least about 100, 150, 200, 250, 300, 350, 400, 450, 500 residues, or the full length of SEQ ID NO:10,

~~an amino acid sequence having at least 50% sequence identity to SEQ ID NO:12 over a region of at least about 100, 150, 200, 250, 300, 350, 400, 450, 500, 550 residues, or the full length of SEQ ID NO:12,~~

~~an amino acid sequence having at least 50% sequence identity to SEQ ID NO:14 over a region of at least about 100, 150, 200, 250, 300, 350, 400, 450 residues, or the full length of SEQ ID NO:14,~~

~~an amino acid sequence having at least 60% sequence identity to SEQ ID NO:16 over a region of at least about 100, 150, 200, 250, 300, 350, 400, 450, 500 residues, or the full length of SEQ ID NO:16,~~

~~an amino acid sequence having at least 50% sequence identity to SEQ ID NO:18 over a region of at least about 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1100, 1200, 1300, 1350 residues, or the full length of SEQ ID NO:18,~~

~~an amino acid sequence having at least 80% sequence identity to SEQ ID NO:20 over a region of at least about 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1100, 1200, 1300, 1400, 1500, 1600, 1650 residues, or the full length of SEQ ID NO:20,~~

~~an amino acid sequence having at least 95% sequence identity to SEQ ID NO:22 over a region of at least about 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1100, 1200, 1300, 1400 residues, or the full length of SEQ ID NO:22, or~~

~~an amino acid sequence having at least 80% sequence identity to SEQ ID NO:24 over a region of at least about 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1100, 1200, 1300, 1400, 1500, 1600, 1650 residues, or the full length of SEQ ID NO:24,~~

wherein optionally the sequence identities are determined by analysis with a sequence comparison algorithm or by a visual inspection,

wherein optionally the sequence comparison algorithm is a BLAST version 2.2.2 algorithm where a filtering setting is set to blastall -p blast, -d "nr pataa" -F F, and all other options are set to default; or

(b) a polypeptide having glucosidase activity encoded by a nucleic acid comprising the sequence of claim 1, or subsequences thereof,

wherein optionally in (a) or (b) the glucosidase activity comprises an .alpha.-glucosidase activity, or the glucosidase activity comprises catalyzing the hydrolysis of an alpha-(1,4) glucose linkage, an alpha-(1,6) glucose linkage, an alpha-(1,2) glucose linkage, an alpha-(1,3) glucose linkage or a combination thereof, or the glucosidase activity comprises catalyzing the hydrolysis of alpha-(1,4) glucose linkages and alpha-(1,6) glucose linkages, or the glucosidase activity comprises hydrolyzing glucosidic bonds in a starch to produce maltodextrins, or the glucosidase activity comprises catalyzing the hydrolysis of both malto-oligosaccharides and liquefied starch, or the .alpha.-glucosidase activity comprises a 1,4-.alpha.-D-glucan hydrolase activity or a 1,6-.alpha.-D-glucan hydrolase activity, or the glucosidase activity comprises an exoglucosidase activity, or the .alpha.-glucosidase activity comprises hydrolyzing glucosidic bonds in a starch, or the glucosidase activity comprises catalyzing the hydrolysis of starch to alpha-D-glucose residues, or the glucosidase activity comprises cleaving a glucose residue from a reducing or a non-reducing end of a starch,

wherein optionally in (a) or (b) the glucosidase activity is thermostable, or the polypeptide retains a glucosidase activity under conditions comprising a temperature range of between about 37° C. to about 95 ° C., or wherein the polypeptide retains a glucosidase activity under conditions comprising a temperature range of between about 55 ° C. to about 85 ° C., between about 70 ° C. to about 95 ° C. or between about 90 ° C. to about 95 ° C.,

wherein optionally in (a) or (b) the glucosidase activity is thermotolerant, or the polypeptide retains a glucosidase activity after exposure to a temperature in the range from between about 37 ° C. to about 95 ° C., or the polypeptide retains a glucosidase activity after exposure to a temperature in the range from between about 55 ° C. to about 85 ° C. or between about 90 ° C. to about 95 ° C.,

wherein optionally the amylase activity comprises a specific activity at about 37 ° C. in the range from about 100 to about 1000 units per milligram of protein, or optionally the amylase activity comprises a specific activity from about 500 to about 750 units per milligram of protein,

wherein optionally the polypeptide comprises at least one glycosylation site, wherein optionally the polypeptide retains an amylase activity under conditions comprising about pH 5, about pH 4.5, about pH 8.0, about pH 8.5, about pH 9, about pH 9.5, about pH 10 or about pH 10.5.

Claims 53 to 71 (canceled)

Claim 72 (previously presented): An isolated or recombinant polypeptide comprising the polypeptide of claim 52 and lacking a signal sequence, or lacking an endogenous signal sequence and comprising a heterologous signal sequence, or further comprising a heterologous peptide or polypeptide, or having a heterologous signal sequence.

Claims 73 to 81 (canceled)

Claim 82 (previously presented): A protein preparation comprising the polypeptide of claim 52, wherein the protein preparation comprises a liquid, a solid or a gel.

Claim 83 (previously presented): A heterodimer comprising the polypeptide of claim 52 and a second domain,

wherein optionally the second domain is a polypeptide and the heterodimer is a fusion protein, or the second domain is an epitope or a tag.

Claims 84 to 85 (canceled)

Claim 86 (previously presented): A homodimer comprising the polypeptide of claim 52.

Claim 87 (previously presented): An immobilized polypeptide or nucleic acid, wherein the

polypeptide comprises the nucleic acid sequence of claim 52, or a subsequence thereof, and the nucleic acid comprises the nucleic acid sequence of claim 1,

wherein optionally the polypeptide is immobilized on a cell, a metal, a resin, a polymer, a ceramic, a glass, a microelectrode, a graphitic particle, a bead, a gel, a plate, an array or a capillary tube.

Claim 88 (canceled)

Claim 89 (withdrawn - previously presented): An array comprising the immobilized polypeptide of claim 87.

Claim 90 (canceled)

Claim 91 (withdrawn - previously presented): An isolated, synthetic or recombinant antibody that specifically binds to the polypeptide of claim 52, wherein the antibody is a monoclonal or a polyclonal antibody.

Claim 92 to 93 (canceled)

Claim 94 (withdrawn - previously presented): A food, a feed, a food supplement or a feed supplement for an animal comprising the polypeptide of claim 52, or a subsequence thereof, wherein optionally the polypeptide is glycosylated.

Claim 95 (canceled)

Claim 96 (withdrawn - previously presented): An edible enzyme delivery matrix comprising the polypeptide of claim 52, wherein optionally the delivery matrix comprises a pellet, or optionally the polypeptide is glycosylated or optionally the polypeptide has a thermotolerant or a thermostable glucosidase activity.

Claim 97 to 102 (canceled)

Claim 103 (withdrawn - previously presented): A method of producing a recombinant polypeptide comprising the steps of: (a) providing a nucleic acid operably linked to a promoter, wherein the nucleic acid comprises the sequence of claim 1; and (b) expressing the nucleic acid of step (a) under conditions that allow expression of the polypeptide, thereby producing a recombinant polypeptide,

wherein optionally the method further comprises transforming an isolated or cultured host cell with the nucleic acid of step (a) followed by expressing the nucleic acid of step (a), thereby producing a recombinant polypeptide in a transformed cell.

Claims 104 to 109 (canceled)

Claim 110 (withdrawn - previously presented): A method for identifying a modulator of a glucosidase activity comprising the following steps:

(a) providing the polypeptide of claim 52;

(b) providing a test compound;

(c) contacting the polypeptide of step (a) with the test compound of step (b) and measuring an activity of the glucosidase, wherein a change in the glucosidase activity measured in the presence of the test compound compared to the activity in the absence of the test compound provides a determination that the test compound modulates the glucosidase activity,

wherein optionally the glucosidase activity is measured by providing a glucosidase substrate and detecting a decrease in the amount of the substrate or an increase in the amount of a reaction product, or, an increase in the amount of the substrate or a decrease in the amount of a reaction product, or

optionally a decrease in the amount of the substrate or an increase in the amount of the reaction product with the test compound as compared to the amount of substrate or reaction product without the test compound identifies the test compound as an activator of glucosidase activity, or

optionally an increase in the amount of the substrate or a decrease in the amount of the reaction product with the test compound as compared to the amount of substrate or reaction product without the test compound identifies the test compound as an inhibitor of glucosidase activity.

Claims 111 to 113 (canceled)

Claim 114 (withdrawn - previously presented): A computer system comprising a processor and a data storage device wherein said data storage device has stored thereon a polypeptide sequence or a nucleic acid sequence, wherein the polypeptide sequence comprises sequence of claim 52, a polypeptide encoded by a nucleic acid of claim 1,

wherein optionally the method further comprises a sequence comparison algorithm and a data storage device having at least one reference sequence stored thereon, and optionally the sequence comparison algorithm comprises a computer program that indicates polymorphisms,

wherein optionally the method further comprises an identifier that identifies one or more features in said sequence.

Claims 115 to 123 (canceled)

Claim 124 (withdrawn – currently amended): A method for isolating or recovering a nucleic acid encoding a polypeptide with a glucosidase activity from an environmental sample comprising the steps of:

(i) (a) providing the amplification primer sequence pair of claim 29;

(b) isolating a nucleic acid from the environmental sample or treating the environmental sample such that nucleic acid in the sample is accessible for hybridization to the amplification primer pair; and,

(c) combining the nucleic acid of step (b) with the amplification primer pair of step (a) and amplifying nucleic acid from the environmental sample, thereby isolating or recovering a nucleic acid encoding a polypeptide with a glucosidase activity from an environmental sample,

wherein optionally each member of the amplification primer sequence pair comprises an oligonucleotide comprising at least about 10 to 50 consecutive bases of a sequence of ~~SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5,~~ SEQ ID NO:9~~, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15 SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23~~, or a subsequence thereof; or

(ii) (a) providing a polynucleotide probe comprising the sequence of claim 1,

(b) isolating a nucleic acid from the environmental sample or treating the environmental sample such that nucleic acid in the sample is accessible for hybridization to a polynucleotide probe of step (a),

(c) combining the isolated nucleic acid or the treated environmental sample of step (b) with the polynucleotide probe of step (a), and

(d) isolating a nucleic acid that specifically hybridizes with the polynucleotide probe of step (a), thereby isolating or recovering a nucleic acid encoding a polypeptide with a glucosidase activity from an environmental sample,

wherein optionally in (i) or (ii) the environmental sample comprises a water sample, a liquid sample, a soil sample, an air sample or a biological sample, and optionally the biological sample is derived from a bacterial cell, a protozoan cell, an insect cell, a yeast cell, a plant cell, a fungal cell or a mammalian cell.

Claims 125 to 128 (canceled)

Claim 129 (withdrawn - previously presented): A method of generating a variant of a nucleic acid encoding a polypeptide with a glucosidase activity comprising the steps of:

(a) providing a template nucleic acid comprising the sequence of claim 1; and

(b) modifying, deleting or adding one or more nucleotides in the template sequence, or a combination thereof, to generate a variant of the template nucleic acid,

wherein optionally the method further comprises expressing the variant nucleic acid to generate a variant glucosidase polypeptide, and optionally the modifications, additions or deletions are introduced by a method comprising error-prone PCR, shuffling, oligonucleotide-directed

mutagenesis, assembly PCR, sexual PCR mutagenesis, in vivo mutagenesis, cassette mutagenesis, recursive ensemble mutagenesis, exponential ensemble mutagenesis, site-specific mutagenesis, gene reassembly, gene site saturation mutagenesis (GSSM), synthetic ligation reassembly (SLR), recombination, recursive sequence recombination, phosphothioate-modified DNA mutagenesis, uracil-containing template mutagenesis, gapped duplex mutagenesis, point mismatch repair mutagenesis, repair-deficient host strain mutagenesis, chemical mutagenesis, radiogenic mutagenesis, deletion mutagenesis, restriction-selection mutagenesis, restriction-purification mutagenesis, artificial gene synthesis, ensemble mutagenesis, chimeric nucleic acid multimer creation and a combination thereof,

wherein optionally the method is iteratively repeated until a glucosidase having an altered or different activity or an altered or different stability from that of a polypeptide encoded by the template nucleic acid is produced, and optionally the variant glucosidase polypeptide is thermotolerant, and retains some activity after being exposed to an elevated temperature, and optionally the variant glucosidase polypeptide has increased glycosylation as compared to the glucosidase encoded by a template nucleic acid, and optionally the variant glucosidase polypeptide has a glucosidase activity under a high temperature, wherein the glucosidase encoded by the template nucleic acid is not active under the high temperature,

wherein optionally the method is iteratively repeated until a glucosidase coding sequence having an altered codon usage from that of the template nucleic acid is produced, and optionally the method is iteratively repeated until a glucosidase gene having higher or lower level of message expression or stability from that of the template nucleic acid is produced.

Claims 130 to 159 (canceled)

Claim 160 (withdrawn - previously presented): A method for hydrolyzing a starch comprising the following steps:

(a) providing a polypeptide having a glucosidase activity, wherein the polypeptide comprises the polypeptide of claim 52, or a polypeptide encoded by the nucleic acid of claim 1;

(b) providing a composition comprising a starch; and

(c) contacting the polypeptide of step (a) with the composition of step (b) under conditions wherein the polypeptide hydrolyzes the starch,

wherein optionally the composition comprises an α-1,4-glucosidic bond or an α-1,6-glucosidic bond.

Claim 161 (canceled)

Claim 162 (withdrawn – previously presented): A method for liquefying or removing a starch from a composition comprising the following steps:

(a) providing a polypeptide having a glucosidase activity, wherein the polypeptide comprises the polypeptide of claim 52, or a polypeptide encoded by the nucleic acid of claim 1;

(b) providing a composition comprising a starch; and

(c) contacting the polypeptide of step (a) with the composition of step (b) under conditions wherein the polypeptide removes or liquefies the starch.

Claims 163 to 165 (canceled)

Claim 166 (previously presented): A detergent composition comprising the polypeptide of claim 52, or a polypeptide encoded by the nucleic acid of claim 1, wherein the polypeptide comprises a glucosidase activity,

wherein optionally the glucosidase is a nonsurface-active glucosidase or a surface-active glucosidase, or optionally the glucosidase is formulated in a non-aqueous liquid composition, a cast solid, a granular form, a particulate form, a compressed tablet, a gel form, a paste or a slurry form.

Claims 167 to 168 (canceled)

Claim 169 (withdrawn - previously presented): A method for washing an object comprising the following steps:

(a) providing a composition comprising a polypeptide having a glucosidase activity, wherein the polypeptide comprises the polypeptide of claim 52, or a polypeptide encoded by a nucleic acid of claim 1;

(b) providing an object; and

(c) contacting the polypeptide of step (a) and the object of step (b) under conditions wherein the composition can wash the object.

Claim 170 (withdrawn - previously presented): A method for hydrolyzing a starch in a feed or a food prior to consumption by an animal comprising the following steps:

(a) obtaining a feed material comprising a starch, wherein the starch can be hydrolyzed by a polypeptide having a glucosidase activity, wherein the polypeptide comprises the polypeptide of claim 52, or a polypeptide encoded by the nucleic acid of claim 1; and

(b) adding the polypeptide of step (a) to the feed or food material in an amount sufficient for a sufficient time period to cause hydrolysis of the starch and formation of a treated food or feed, thereby hydrolyzing the starch in the food or the feed prior to consumption by the animal,

wherein optionally the food or feed comprises rice, corn, barley, wheat, legumes, or potato.

Claim 171 (canceled)

Claim 172 (withdrawn - previously presented): A feed or a food comprising the polypeptide of claim 52, or a polypeptide encoded by the nucleic acid of claim 1.

Claim 173 (withdrawn - previously presented): A composition comprising a starch and the polypeptide of claim 52, or a polypeptide encoded by the nucleic acid of claim 1.

Claim 174 (withdrawn - previously presented): A textile comprising the polypeptide of claim 52, or a polypeptide encoded by the nucleic acid of claim 1.

Claim 175 (withdrawn - previously presented): A method for textile desizing comprising the following steps:

(a) providing a polypeptide having a glucosidase activity, wherein the polypeptide comprises the polypeptide of claim 52, or a polypeptide encoded by the nucleic acid of claim 1;

(b) providing a fabric; and

(c) contacting the polypeptide of step (a) and the fabric of step (b) under conditions wherein the glucosidase can desize the fabric.

Claim 176 (withdrawn - previously presented): A paper or paper product or paper pulp comprising the polypeptide of claim 52, or a polypeptide encoded by the nucleic acid of claim 1.

Claim 177 (withdrawn - previously presented): A method for deinking of paper or fibers comprising the following steps:

(a) providing a polypeptide having a glucosidase activity, wherein the polypeptide comprises the polypeptide of claim 52, or a polypeptide encoded by the nucleic acid of claim 1;

(b) providing a composition comprising paper or fiber; and

(c) contacting the polypeptide of step (a) and the composition of step (b) under conditions wherein the polypeptide can deink the paper or fiber.

Claim 178 (withdrawn - previously presented): A method for treatment of lignocellulosic fibers comprising the following steps:

(a) providing a polypeptide having a glucosidase activity, wherein the polypeptide comprises the polypeptide of claim 52, or a polypeptide encoded by the nucleic acid of claim 1;

(b) providing a lignocellulosic fiber; and

(c) contacting the polypeptide of step (a) and the fiber of step (b) under conditions wherein the polypeptide can treat the fiber thereby improving the fiber properties.

Claim 179 (withdrawn - previously presented): A high-maltose or a high-glucose liquid or syrup comprising the polypeptide of claim 52, or a polypeptide encoded by the nucleic acid of claim

1.

Claim 180 (withdrawn - previously presented): A method for producing a high-maltose or a high-glucose syrup comprising the following steps:

(a) providing a polypeptide having a glucosidase activity, wherein the polypeptide comprises the polypeptide of claim 52, or a polypeptide encoded by the nucleic acid of claim 1;

(b) providing a composition comprising a starch; and

(c) contacting the polypeptide of step (a) and the composition of step (b) under conditions wherein the polypeptide of step (a) can hydrolyze the composition of step (b), thereby producing a high-maltose or a high-glucose syrup,

wherein optionally the starch is from rice, corn, barley wheat, legumes, potato, or sweet potato.

Claim 181 (canceled)

Claim 182 (withdrawn - previously presented): A method for improving the flow of the starch-containing production fluids comprising the following steps:

(a) providing a polypeptide having a glucosidase activity, wherein the polypeptide comprises the polypeptide of claim 52, or a polypeptide encoded by the nucleic acid of claim 1;

(b) providing production fluid comprising a starch; and

(c) contacting the polypeptide of step (a) and the production fluid of step (b) under conditions wherein the glucosidase can hydrolyze the starch in the production fluid, thereby improving its flow by decreasing its density,

wherein optionally the production fluid is from a subterranean formation.

Claim 183 (canceled)

Claim 184 (withdrawn - previously presented): An anti-staling composition comprising the polypeptide of claim 52, or a polypeptide encoded by the nucleic acid of claim 1.

Claim 185 (withdrawn - previously presented): A method for preventing staling of a baked product comprising the following steps:

(a) providing a polypeptide comprising the polypeptide of as set forth claim 52, or a polypeptide encoded by the nucleic acid of claim 1;

(b) providing a composition used for baking comprising a starch;

(c) combining the polypeptide of step (a) with the composition of the step (b) under conditions wherein the polypeptide can hydrolyze the starch in the composition used for baking, thereby preventing staling of the baked product,

wherein optionally the baked product is a bread or a bread product.

Claim 186 (canceled)

Claim 187 (withdrawn - previously presented): A method for using glucosidase in brewing or alcohol production comprising the following steps:

(a) providing a polypeptide comprising the polypeptide of claim 52, or a polypeptide encoded by the nucleic acid of claim 1;

(b) providing a composition used for brewing or in alcohol production comprising a starch or a polysaccharide;

(c) combining the polypeptide of step (a) with the composition of the step (b) under conditions wherein the polypeptide can hydrolyze the starch or the polysaccharide in the composition used for brewing or alcohol production,

wherein optionally the composition comprises starch or the polysaccharide is a beer.

Claim 188 (canceled)

Claim 189 (withdrawn - previously presented): An alcoholic beverage comprising the polypeptide of claim 52, or a polypeptide encoded by the nucleic acid of claim 1.

Claim 190 (withdrawn - previously presented): A beer comprising the polypeptide of claim 52, or a polypeptide encoded by the nucleic acid of claim 1.

Claim 191 (previously presented): A pharmaceutical composition comprising the polypeptide of claim 52, or a polypeptide encoded by the nucleic acid of claim 1.

Claims 192 to 206 (canceled)

Claim 207 (withdrawn – currently amended): An isolated, synthetic or recombinant signal sequence: (a) consisting of a sequence as set forth in residues 1 to 16, 1 to 17, 1 to 18, 1 to 19, 1 to 20, 1 to 21, 1 to 22, 1 to 23, 1 to 24, 1 to 25, 1 to 26, 1 to 27, 1 to 28, 1 to 28, 1 to 30 or 1 to 31, 1 to 32 or 1 to 33 of: (i) the amino acid sequence of claim 52, or (ii) the amino acid sequence of ~~SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8,~~ SEQ ID NO:10, ~~SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22 or SEQ ID NO:24~~; or (b) comprising a sequence as set forth in residues 1 to 16, 1 to 17, 1 to 18, 1 to 19, 1 to 20, 1 to 21, 1 to 22, 1 to 23, 1 to 24, 1 to 25, 1 to 26, 1 to 27, 1 to 28, 1 to 28, 1 to 30 or 1 to 31, 1 to 32 or 1 to 33 of: (i) the amino acid sequence of claim 52, or (ii) the amino acid sequence of ~~SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:11~~ SEQ ID NO: 10~~, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22 or SEQ ID NO:24~~.

Claim 208 (canceled)

Claim 209 (previously presented): A chimeric protein comprising a first domain comprising a signal sequence as set forth in claim 207 and at least a second domain, wherein optionally the protein is a fusion protein, or optionally the second domain comprises an enzyme, or optionally the enzyme is a glucosidase.

Claims 210 to 212 (canceled)

Claim 213 (previously presented): A chimeric polypeptide comprising at least a first domain comprising signal peptide (SP) having a sequence as set forth in claim 207, and at least a second domain comprising a heterologous polypeptide or peptide, wherein the heterologous polypeptide or peptide is not naturally associated with the signal peptide (SP),

wherein optionally the heterologous polypeptide or peptide is not a glucosidase, or optionally the heterologous polypeptide or peptide is amino terminal to, carboxy terminal to or on both ends of the signal peptide (SP) or a catalytic domain (CD).

Claims 214 to 215 (canceled)

Claim 216 (withdrawn - previously presented): An isolated or recombinant nucleic acid encoding a chimeric polypeptide, wherein the chimeric polypeptide comprises at least a first domain comprising signal peptide (SP) having a sequence as set forth in claim 213 and at least a second domain comprising a heterologous polypeptide or peptide, wherein the heterologous polypeptide or peptide is not naturally associated with the signal peptide (SP).

Claim 217 (withdrawn - previously presented): An oral care product comprising a polypeptide as set forth in claim 52, or a polypeptide encoded by a nucleic acid as set forth in claim 1,

wherein optionally the product comprises a toothpaste, a dental cream, a gel or a tooth powder, an odontic, a mouth wash, a pre- or post brushing rinse formulation, a chewing gum, a lozenge or a candy.

Claim 218 (canceled)